AMENDMENTS

Please amend the above-identified U.S. Application No. 09/851,873 as follows:

In the Specification

At page 14, beginning at line 5 and ending at page 15, line 3, please replace the paragraphs describing Figures 1, 2, 3, 4 and 5 with the following paragraphs:

Figure 1A through Figure 1B shows an alignment of the amino acid sequences of a human caspase-12 isoform designated KW-A (SEQ ID NO: 4) with other members of the caspase family: human caspase-1 (SEQ ID NO: 80), putative human caspase-13 (SEQ ID NO: 81), human caspase-4 (SEQ ID NO: 82), human caspase-5 (SEQ ID NO: 83), mouse caspase-12 (SEQ ID NO: 84) and mouse caspase-11 (SEQ ID NO: 85). Legend: [a]translated amino acid sequence from putative human caspase 13 in EMBL database; [b]"*" means amino acid is identical for all sequences; ":" means amino acids are considered conservative substitutions among all sequences; "." means amino acids may be considered conservative substitutions among all sequences.

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Figure 3A through Figure 3B shows an alignment of a non-naturally occurring variant human caspase-12 isoform, designated hCaspase-12 (SEQ ID NO: 77) in the Figure and described in more detail in Example 3B below, with murine caspase-12 (SEQ ID NO: 84). *Legend for Domains as calculated by PFAM:* CARD Domain = XXXXXXX; ICE-p20 Domain: YYYYYYY; ICE-p10 Domain: ZZZZZZZ; Active-Site Residues: **H**...**C**; Calpain and Auto-

catalytic cleavage sites determined for Mouse Caspase-12.

Figure 4A through Figure 4E shows an alignment of the amino acid sequences of the non-naturally occurring variant hCaspase-12 (SEQ ID NO: 77), murine caspase-12 (SEQ ID NO: 84), human caspase-1 (SEQ ID NO: 80), human caspase-2 (SEQ ID NO: 97), human caspase-3 (SEQ ID NO: 98), human caspase-4 (SEQ ID NO: 82), human caspase-5 (SEQ ID NO: 83), human caspase-6 (SEQ ID NO: 99), human caspase-7 (SEQ ID NO: 100), human caspase-8 (SEQ ID NO: 101), human caspase-9 (SEQ ID NO: 102), human caspase-10 (SEQ ID NO: 103), human caspase-13 (SEQ ID NO: 104), and human caspase-14 (SEQ ID NO: 105).

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Figure 5A through Figure 5B shows an alignment of the amino acid sequences of hCaspase-12 (SEQ ID NO: 77) and the most closely related human caspases, caspase-4, -5, -13 and -1.

Please replace the paragraph beginning at page 86, line 3 and ending at page 87, line 4, with the following paragraph, which inserts a sequence identifier for EMBL Accession No. O08736:

The cDNA encoding human caspase-12 was cloned as follows. Comparison of all of the known caspases from mammalian, vertebrate, and invertebrate species to sequences in the Celera database identified a number of partial human DNA sequences. Some of these DNA sequences, ga_7598929 (SEQ ID NO: 30), ga_7683974 (SEQ ID NO: 31), ga_9453932 (SEQ ID NO: 32), ga_9504136 (SEQ ID NO: 33), ga_12715389 (SEQ ID NO: 34), ga_13398395 (SEQ ID NO: 35), ga_13611202 (SEQ ID NO: 36), ga_15018831 (SEQ ID NO: 37), and ga_15856828 (SEQ ID NO: 38) showed homology to murine caspase-12 (EMBL Accession No. O08736; SEQ ID NO: 84) as well as human caspase-4 and human caspase-5. Programs such as Bestfit, Compare/Dotplot, Extractpeptide, Findpatterns, GAP, Lineup, Map, Motifs and Pileup (GCG Package referenced above) were used to analyze and translate the nucleotide sequences. These nucleotide sequences were translated and modified (to eliminate an internal stop codon) to optimize homology to the murine caspase-12 sequence. The optimized portion of the amino acid sequence corresponding to ga_7598929 (SEQ ID NO: 30) is set forth in SEQ ID NO: 39, the

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